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IMPACT OF ENSEMBLE LEARNING ALGORITHMS TOWARDS ACCURATE HEART DISEASE PREDICTION

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Abstract

The medical field comprises of various techniques. Yet, the Data mining is playing a crucial role in determining the future of medications and patients' state. This is because of the reliability offered by the various classification techniques. Still, accurate prediction of heart disease is becoming more and more challenging due to the influence of the various factors extracted from patients. Identifying these factors is a crucial research task. In such a scenario, the individual classification algorithms fail to produce perfect models capable of accurately predicting the heart disease. Hence, by introducing the ensemble learning methods, higher performance could be achieved leading to the accurate prediction of heart diseases. In this research work, the performance of the three ensemble classifiers namely Bagging, Stacking and AdaBoost is experimented and evaluated on various folds of cross validation with benchmark dataset for heart disease prediction. The base learners considered for constructing the ensemble are well known classifiers namely Support Vector Machine, Naive Bayes and K-Nearest Neighbour. The results illustrate the improved performance in terms of performance metrics and provide a better understanding of the accuracy, reliability and usefulness of the ensemble models in favouring improved performance for heart disease prediction.

Keywords:
Heart Disease, Patient Health, Prediction, Classification, Ensemble Classifier, Data Mining

1. INTRODUCTION

Traditionally, the heart diseases problems have been most common in our society. The prediction of those types of diseases is very common and several measures are practiced day to day. Normally, there are many factors that affect a human heart such as genetic factors through which a type of heart disease is passed down from generations. According to the World Health Organization, every year more than 12 million of deaths are occurring worldwide due to the various types of heart diseases which are also known by the term cardiovascular disease.

The possibility of heart disease among young may increase due to the bad eating habits, lack of sleep, depression, obesity, family history, high blood pressure, high blood cholesterol, smoking and hypertension. The discomfort felt by the individual defines the heart disease type. Some symptoms are not usually identified by the common people.

The common symptoms for heart diseases include breathlessness, shoulder pain, chest pain, and heart palpitations. Angina or angina pectoris is a type of heart disease that mainly triggers when a part of the heart does not receive enough oxygen. Other symptoms of angina include pain that travels through the body, for example from the chest to the arms, neck, back, abdomen, or jaw, light headedness and dizzy sensations, profuse sweating, nausea and vomiting.

Heart failure is also an outcome of heart disease, and breathlessness can occur when the heart becomes too weak to circulate blood. Some heart conditions occur with no symptoms at all, especially in older adults and individuals with diabetes. When these circumstances are considered, the healthcare industry needs to store additional data about the patients and their medications for generating diagnosis report.

The advancement in the computing and storage technologies have empowered the healthcare industry to collect and store routine medical data aiding to the increased and constant support in medical decisions. In many developed countries, the patients' data are collected and stored in digital form. The data is then analysed to make the necessary medical decisions involving prediction, diagnosis, image analysis, and line of treatment. Machine learning and Data Mining algorithms have been playing a vital role in solving complex, highly nonlinear classification and prediction problems.

The classification is one data mining technique through which the future outcome or predictions can be seen. Machine learning plays a major role in identifying the type of heart disease based on the huge data. Data Mining is a machine learning task that is utilized for extracting vital information from the data. More specifically, it helps in the decision making process that is done based on a collection of past records.

In Data Mining, the classification commonly represented as supervised machine learning is used for making future outcomes based on the historical data. Medical data mining utilizes the data mining technique such as classification and provides insights based on the data and presents medical outcomes. It is possible to provide insights on a patient's history and is able to provide clinical support through the analysis. The classification algorithms can be trained and tested to make the predictions that determining the person's nature of being affected by heart disease. But, due to the intensity of the medical problem being high, the solution demands higher levels of classification accuracy. Traditional classification algorithms fail to provide them. In such a case, the Ensemble methods may be used. More specifically, for identification of the heart disease the ensemble classification algorithms that combine two or more classification techniques and produce the best predictive result.

In this research work, the family of ensemble classification techniques is utilized for making the heart disease predictions. A comparative analysis of the three ensemble classification algorithms namely Bagging, Stacking and AdaBoost are used to make predictions. The analysis done using the algorithms varies from several various folds of cross validation on the StatLog heart disease benchmark dataset obtained from UCI machine learning repository. This final model can be used for predicting any type of heart disease and the evaluation results present the best ensemble classification algorithm suitable for heart disease prediction.

2. LITERATURE REVIEW

Based on the study given by Carlos Ordonez, the heart disease can be predicted with some basic attributes taken from the patient and in their work have introduced a system that includes the characteristics of an individual human being based on totally 13 basic attributes like sex, blood pressure, cholesterol and others to predict the likelihood of a patient getting affected by heart disease. They have added two more attributes i.e. fat and smoking behaviour and extended the research dataset. The data mining classification algorithms such as Decision Tree, Naive Bayes, and Neural Network are utilized to make predictions and the results are analysed on Heart disease database.

Eibe Frank et al. [3] have done a research work which contains an extensive collection of machine learning algorithms and data pre-processing methods that is processed by a GUI for data exploration and the experimental comparison of different machine learning techniques on the same problem. By using Weka, they were able to easily identify a suitable ensemble algorithm for generating an accurate predictive model from it. Duff, et al. [4] has done a research work involving 530 patients having cardiac arrest and they were added to the analysis of heart disease probabilities. They used Bayesian networks for statistical analysis and data mining analysis.

Frawley and Shapiro [9] have taken a challenging research problem for medical society and performed a prediction of survival of Coronary heart disease (CHD). They utilized 10-fold cross-validation methods for performance comparison purposes. Parthiban and Subramanian [6] have proposed a new work in which the heart disease is identified and predicted using the proposed Coactive Neuro-Fuzzy Inference System (CANFIS). Their model works based on the collective nature of neural network adaptive capabilities and based on the genetic algorithm along with fuzzy logic. The performance of the proposed CANFIS model was evaluated. As a result, the proposed CANFIS model showed great prospective in predicting the heart disease. Singh and Singh [7] have done a work using, one partition clustering algorithm (K-Means) and one hierarchical clustering algorithm (agglomerative). K-means algorithm has higher effectiveness and scalability and converges fast when production with large data sets. Hierarchical clustering constructs a hierarchy of clusters by either frequently merging two smaller clusters into a larger one or splitting a larger cluster into smaller ones. Using WEKA data mining tool, they have calculated the performance of k-means and hierarchical clustering algorithm on the basis of accuracy and running time.

Palaniappan and Awang [8] have carried out a research work and have built Intelligent Heart Disease Prediction System (IHDPS) by the application of several data mining techniques such as Decision Trees, Neural Network and Naïve Bayes. Breiman [1] has written an article on bagging predictors. His work describes the method for generating multiple versions of a predictor for getting an aggregated predictor. When predicting the class as numerical outcome, the aggregation is averaged. When it’s a nominal outcome, the plurality vote is considered when predicting a class. The multiple versions are formed by making bootstrap replicates of the learning set and using these as new learning sets. Tests on real and simulated data sets using classification and regression trees and subset selection in linear regression show that bagging can give substantial gains in accuracy.

Hsieh et al. [5] have proposed an ensemble classifier for credit scoring system by utilizing several data mining techniques with binning to discretize the continuous values through the use of optimal associate binning. The ensemble includes neural network, support vector machine, and Bayesian network. The knowledge obtained from the classifier is represented in multiple forms such as causal diagram and constrained association rules.

Yanwei, et al. [10] have built a classification method based on the origin of multi parametric features by assessing HRV (Heart Rate Variability) from ECG and the data is pre-processed and heart disease prediction model is built that classifies the heart disease of a patient.

Miao et al. [11] has discovered a method for utilizing ensemble learning for heart disease prediction. They identified that the heart disease is the leading cause of death for both men and women. One in every four people is afflicted with and dies of heart disease. Early and accurate diagnoses of heart disease thus are crucial in improving the chances of long-term survival for patients

Das et al. [12] performed a research work in which they have evaluated the performance of three popular ensemble methods for the diagnosis of the valvular heart disorders. They have presented a comparative study by using a data set containing 215 samples to evaluate the performance of investigated ensemble methodology. Yekkala et al. [13] presented a diverse analysis of various ensemble methods (Bagged Tree, Random Forest, and AdaBoost) along with Feature subset selection method - Particle Swarm Optimization (PSO), to accurately predict the occurrence of heart disease for a particular patient. Experimental results show that Bagged Tree and PSO achieved the highest accuracy.

Ekiz et al. [14] conducted an experiment to classify heart disease both in MATLAB environment and WEKA, by using six different algorithms. Linear SVM, Quadratic SVM, Cubic SVM, Medium Gaussian SVM, Decision Tree and Ensemble Subspace Discriminant machine learning approaches were used for predicting the occurrence of heart disease. Raza [15] presented a research in which different machine learning techniques have been ensembled using the majority voting technique to predict heart diseases that obtained accuracy of 88.88%. David and Belcy [16] presented a data mining technique for comparing three data mining classification algorithms like Random Forest, Decision Tree and Naïve Bayes and the results are addressed to develop a prediction system in order to analyse and predict the possibility of heart disease. These algorithms are a standard and have already been discussed by David et al. [17] in predicting the medical domain for predicting the brain tumour. The similar concept is studied from the concept of extracting features that are used to train and build a classification model using the classification algorithms such as Naïve Bayes, K-Nearest Neighbour and Multi-class Support Vector Machine. Similarly, towards ensemble prediction David and Suruliandi [18] has presented a model that aids in the generation involving multiple equal splits of datasets that are used to get the final estimation. These generated ensemble methods conceal the disadvantage of those single models generated from the individual predictors and improve the overall performance to provide the best prediction possible

Li et al. [2] identified that the imbalance of the data on a dataset is due to a large number of missing values. They presented a new prediction model of AdaBoost and Random Forest that is constructed by using the information gain ratio to analyse the feature contribution degree of the dataset.

3. MOTIVATION AND JUSTIFICATION

The main motivation of doing this research is to present a heart disease prediction model using the ensemble learning classification algorithms for the best prediction of heart disease occurrence. Further, this research work is aimed towards identifying the best ensemble classification algorithm for identifying the possibility of heart disease in a patient. This work is justified by performing a comparative study and analysis using three ensemble classification algorithms namely Bagging, Stacking and AdaBoost that are evaluated at various levels of cross folding that explicitly presents the best ensemble learning algorithm. This in-turn provides researchers and medical practitioners to establish a better understanding of the heart disease prediction and help them identify a solution towards prediction of heart diseases.

3.1 DATASET DESCRIPTION

The database for this research work has been taken from the StatLog dataset in UCI repository. It includes 13 attributes. The heart disease dataset included in this research work consists of total 270 instances with no missing values. The dataset is typically used for various types of heart diseases such as typical angina, atypical angina, and non-anginal pain and asymptomatic. This research work is aimed at predicting the heart disease irrelevant of the disease types. The attribute is a numeric data type that represents the age of the patient and ranges from 29 to 65 years. The Cp is an attribute for determining the pain type, represented from the range1 to 4. The trestbps is a resting blood pressure that lies between 92 and 100; the fbs is fasting blood sugar level that is either a 1 or 0 representing Boolean values true or false. The restecg is the resting electro cardio graphic result represented as three cases from 0 to 2. The thalach is the maximum heart rate achieved ranging from 82 to 185. The exang is the exercise induced angina that is a Boolean value. The disease is the target class of the dataset denoting the heart disease presence with a yes or a number. Similarly, all the attributes and their values are represented in Table.1.

Table.1. Attribute and Description of the dataset used for research

Attribute name	Type	Description	Range
Age	Numeric	Age in years	29-65
Cp	Nominal	Chest pain type	typical angina = 1, atypical angina = 2, non-anginal pain = 3, asymptomatic = 4
trestbpd	Numeric	Resting blood pressure	92-200
fbs	Nominal	Fasting blood sugar level	Yes =1, No = 0
restecg	Nominal	Resting electrocardiographic results	Normal = 0, having ST-T wave abnormality=1, showing probable or definite left ventricular hypertrophy = 2
thalach	Numeric	Maximum heart rate achieved	82-185
exang	Numeric	Exercise induced angina	Yes =1, No = 0
Disease	Nominal	Identification of a heart disease.	Yes, No

4. METHODOLOGY

The heart disease prediction can be performed by following the procedure which is similar to Fig.1 which specifies the research methodology for building a classification model required for the prediction of the heart diseases in patients.

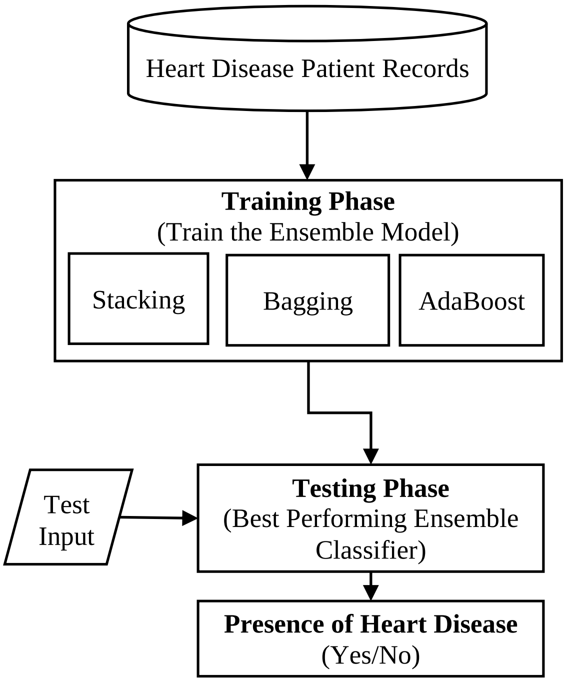

Fig.1. Methodology of Ensemble Learning for Heart Disease Prediction

The model forms a fundamental procedure for carrying out the heart disease prediction using ensemble machine learning techniques. In order to make predictions, an ensemble classifier needs to be trained with the records and then produce a classification model. The model is further used to make the predictions for identifying the unknown instance. The research methodology of this research includes the performance evaluation of the three ensemble classification algorithms by using cross validation. In the cross validation, the training and testing data is split up from the heart disease using several folds such as 10 folds wherein each fold is recursively used for training and testing by replacement in the dataset for testing and training. In this work, the training phase includes training the three ensemble classification algorithms namely Bagging, Stacking and AdaBoost using the heart disease dataset and a classification model is built. All the three algorithms are described in the sections given below.

4.1 CLASSIFICATION USING ADABOOST

AdaBoost [9] which is shortened from Adaptive Boosting is a machine learning meta-algorithm which could be used alone with many different types of learning algorithms in order to improve the performance. The output of constituting learning algorithms is then combined as a weighted sum that represents the final output of the boosted classifier. The word adaptive refers to the algorithm's nature of tweaking the subsequent weak learners in the favour of those instances that are misclassified by previous classifiers in the list. Hence, the AdaBoost is sensitive to noisy data and outliers. A generalized algorithm for the AdaBoost is given below.

```
Sample - $S_1, S_2, S_3 \ldots\ldots S_n$
Desired output - Predicted Class {-1,+1}
Initial weights - $w_1, w_2, w_3, \ldots, w_n$
Error Function - $f$
Weak learners - $c_1, c_2, c_3, .., c_n$
Step 1: For each Classifier x in Total Classifiers ($T$)
Step 2:     Choose $h_1(x)$
Step 3:     Find weak learners that minimizes the weighted sum error for misclassified points
                a. Add to Ensemble
                b. Update Weights and coefficients
Step 4: End for
Step 5: Based on coefficients with biased weights, the final desired output is produced.
```

4.2 CLASSIFICATION USING BAGGING

Bagging [1] termed as Bootstrap aggregating is a meta-learning machine learning algorithm that is designed to improve the stability and accuracy of machine learning algorithms used in statistical classification and regression. Although bagging is known to be applied with the decision tree methods, it can also be used with any type of classification methods. Bagging follows a model averaging approach and it also decreases the variance amount in order to avoid over fitting of the data. The generalized algorithm for Bagging is given below.

```
Number of models - $N$
Sample with replacement - $X$
Classification Algorithm - $C$
Trained Models - $m_1, m_2, m_3, \ldots\ldots, m_N$
Desired output - ($E$) i.e. Predicted Class {-1,+1}
Step 1: For each model untrained
            a. Train a Classification algorithm $C$ on this sample
            b. Save the model $m_i$
Step 2: End For
Step 3: Estimate from each models in $m$
Step 4: Average the estimates to produce $E$.
```

4.3 CLASSIFICATION USING STACKING

Stacked Generalization or stacking [11] also known as meta-ensemble is a model ensembling technique that is used to combine the results from multiple predictive models to generate a new model out from the results. In many cases, this will improve the accuracy of the prediction when compared with the individual models that are generated from its composite algorithms. It also eliminates the results of the classifier which are poor. The predictions from the existing models or sub-models are combined using a new model and referred to as blending which combines random subspace and gradient descent. Models that have their predictions combined must have skill on the problem, but do not need to be the best possible models. The following steps describe the working procedure of Stacking.

```
Step 1: Train each of the $L$ base algorithms on the training set.
Step 2: Perform $k$-fold cross-validation on each of these learners and collect the cross-validated predicted models $m_1$ to $m_N$ from each of the $L$ algorithms.
Step 3: The $N$ cross-validated predicted values from each of the $L$ algorithms can be combined to form a new $N \times L$ matrix.
Step 4: Train the meta-learning algorithm data.
Step 5: Construct the ensemble model with $L$ base learning models and the meta-learning model $Z$
Step 6: Generate ensemble predictions $U$ from the predictions of base learners.
Step 7: Feed prediction models into the meta-learner $Z$ to generate the ensemble prediction using logistic regression.
```

5. PERFORMANCE METRICS

The metrics used for the research work is described in this section.

Precision: Precision is the part of significant instances between the retrieved instances. The equation of precision is given in Eq.(1).

$$Precision = TP/(TP+FP) \quad (1)$$

Recall: Recall is the small part of appropriate instances that have been retrieved over the total quantity of relevant instances. The equation of recall is given in Eq.(2)

$$Recall = TP/(TP+FN) \quad (2)$$

F-Measure: The f-score (or f-measure) is considered based on the two times the precision times recall divided by the sum of precision and recall. The equation of F-Measure is given in Eq.(3)

$$F\text{-}Measure = (2*Precision*Recall)/(Precision + Recall) \quad (3)$$

ROC Area: ROC curves are commonly used to show in a graphical way the connection/ trade off involving clinical sensitivity and specificity for every potential cut off for a test or an arrangement of tests.

PRC Area: The Precision-recall curves are not impacted by the count of patients without disease and with low test results. It is extremely suggested to use precision-recall curves as a supplement to the regularly used ROC curves to obtain the full picture when evaluating and comparing.

5.1 EXPERIMENTAL RESULTS

The analysis and identification of the best classification algorithm in this research work is done and the results are provided here. For the validation of the results, several range of experiments are carried out using Cross validation and are described in the section given below.

5.2 CLASSIFICATION USING CROSS VALIDATION

In *k*-fold cross-validation, the innovative sample is randomly partitioned into *k* subsamples. Then *k* subsamples, a single subsample is retained as the validation data designed for testing the representation, and the remaining *k*-1 subsamples are used as training data. This kind of situation is referred to as use training set generally referring to as entirely utilizing the dataset for training and testing. For instance, in 10-fold cross validation, the original sample is randomly partitioned into 10 subsamples. From the 10 subsamples, a single subsample is retained as the validation data i.e. testing data which is used for testing the model and the remaining 9 subsamples is treated as training data that is used for training the classification algorithm. The cross validation process is then repeated in the same manner for 10 times (the folds), with each of the 10 subsamples used exactly once as the validation data. By shuffling and swapping the folds of data, the 10 results from the folds then can be averaged (or otherwise combined) to produce a single estimation. The experimental results of the classification of heart disease done using many folds of cross validation are given in Table.2. Here, *A* refers to the ensemble classification algorithms and *F* refers the number of folds in cross validation.

Table.2. Classification of heart disease using cross validation

A	F	Metrics						
		TP	FP	Precision	Recall	F-measure	ROC	PRC
Stacking	2	0.56	0.56	0.313	0.56	0.402	0.498	0.506
	5	0.56	0.56	0.313	0.56	0.402	0.488	0.501
	8	0.56	0.56	0.313	0.56	0.402	0.481	0.497
	10	0.56	0.56	0.313	0.56	0.402	0.482	0.498
Bagging	2	0.775	0.24	0.775	0.775	0.774	0.787	0.747
	5	0.785	0.241	0.788	0.785	0.781	0.821	0.797
	8	0.775	0.23	0.775	0.775	0.775	0.802	0.751
	10	0.77	0.241	0.77	0.77	0.77	0.819	0.774
AdaBoost	2	0.796	0.219	0.798	0.785	0.791	0.86	0.842
	5	0.804	0.2	0.808	0.804	0.809	0.864	0.847
	8	0.802	0.202	0.803	0.801	0.797	0.861	0.841
	10	0.812	0.187	0.812	0.806	0.802	0.864	0.848

Based on the Table.2, it is understood that the folds for cross validation play a vital role in the improvement of the metric values for the precision, recall and f-measure. Although the performance has been improved based on implementation of several folds, the AdaBoost algorithm outperforms the bagging and stacking algorithms.

6. CONCLUSION AND FUTURE WORK

The main objective of the research work is to identify the best performing ensemble classification algorithm for heart disease prediction. For this purpose, the UCI data repository is used for performing the comparative analysis of three algorithms such as AdaBoost, Bagging and Stacking. From the research work, it has been experimentally proven that AdaBoost provides perfect results as compared to competitors.

The future work of this research work can be made to produce an impact in the accuracy of the Ensemble learning algorithm by altering the procedure for building ensemble models based on the data. The actual data used for heart disease may be changed based on patient history and patient real-time characteristics. Further, by applying genetic algorithm, the parameters of the AdaBoost could be fine-tuned in order to reduce the feature subset for acquiring the optimal subset of attribute that is enough for heart disease prediction. The heart disease prediction can be automated using actual real time data from health care organizations and agencies which can be built using big data.

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